

Detail Description Paragraph:

[0045] The terms ".alpha.-1,3/4-fucosyltransferase or fucosyltransferase" or a nucleic acid encoding an ".alpha.-1,3/4-fucosyltransferase or fucosyltransferase" refer to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater amino acid sequence identity, preferably over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acids, to a polypeptide encoded by a nucleic acid selected from SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, or SEQ ID NO:19; or an amino acid sequence of SEQ ID NO:2; SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, or SEQ ID NO:20; (2) specifically bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence of SEQ ID NO:2; SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, or SEQ ID NO:20; immunogenic fragments thereof, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid encoding SEQ ID NO:2; SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, or SEQ ID NO:20; e.g., a nucleic acid sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, or SEQ ID NO:19; or its complement, and conservatively modified variants thereof; (4) have a nucleic acid sequence that has greater than about 90%, preferably greater than about 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher nucleotide sequence identity, preferably over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, or SEQ ID NO:19; or its complement. The nucleic acids and proteins of the invention include both naturally occurring or recombinant molecules.

<!--StartFragment-->RESULT 4

ADJ77816

ID ADJ77816 standard; protein; 277 AA.

XX

AC ADJ77816;

XX

DT 06-MAY-2004 (first entry)

XX

DE Helicobacter pylori strain 19C2 FutB protein SeqID 8.

XX

KW FutA; FutB; alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid;

KW fucose; N-acetylglucosamine; glycoconjugate; enzyme.

XX

OS Helicobacter pylori.

XX

PN WO2004009838-A2.

XX

PD 29-JAN-2004.

XX

PF 23-JUL-2003; 2003WO-US023057.

XX

PR 23-JUL-2002; 2002US-0398156P.

PR 08-NOV-2002; 2002US-0424894P.

XX

PA (NEOS-) NEOSE TECHNOLOGIES INC.

XX

PI Johnson KF, Bezila DJ;

XX

DR WPI; 2004-123401/12.

DR N-PSDB; ADJ77815.

XX

PT New isolated polynucleotide encoding fucosyltransferase protein, useful

PT for synthesizing oligosaccharide moiety on a protein or lipid that is

PT unglycosylated in its native form or for synthesizing glycolipids.

XX

PS Claim 16; SEQ ID NO 8; 72pp; English.

XX

CC This invention relates to novel isolated polynucleotides and the encoded

CC polypeptides thereof, which are related to the fucosyltransferase enzymes

CC (FutA and FutB) of Helicobacter pylori (H. pylori). Specifically, it

CC refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to

CC chemically synthesize glycoproteins and glycolipids with the desired

CC oligosaccharide moieties (i.e. by transfer of a fucose residue to N-

CC acetylglucosamine), such that they are useful in the preparation of

CC glycoconjugates. The present invention describes how bacterial

CC fucosyltransferase is unaffected by the sialylation status of the acceptor

CC sugar, as opposed to the mammalian homologue, and furthermore,

CC bacterially expressed enzymes offer a large cost saving relative to

CC mammalian expression systems. This polypeptide sequence is an H. pylori

CC strain 19C2 FutB protein sequence of the invention.

XX

SQ Sequence 277 AA;

Query Match 15.2%; Score 68; DB 8; Length 277;

Best Local Similarity 100.0%; Pred. No. 1.5e-57;

Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 73 NPLGSARKILSYQNAKRVFYTGNEVPNFNLFDYAI GFDELDFRDRYLRMPLYYDRLHHK 132

Db 74 NPLGSARKILSYQNAKRVFYTGNEVPNFNLFDYAI GFDELDFRDRYLRMPLYYDRLHHK 133

Qy 133 AESVNDDT 140  
| | | | | |

Db 134 AESVNDDT 141

<!--EndFragment-->

<!--StartFragment-->RESULT 5  
ADJ27351  
ID ADJ27351 standard; protein; 277 AA.  
XX  
AC ADJ27351;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Alpha-1,3/4-fucosyltransferase coding sequence.  
XX  
KW alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase;  
KW fucosyl; fucose.  
XX  
OS Helicobacter pylori; strain 19C2 FutB.  
XX  
PN WO2004009793-A2.  
XX  
PD 29-JAN-2004.  
XX  
PF 23-JUL-2003; 2003WO-US023155.  
XX  
PR 23-JUL-2002; 2002US-0398156P.  
PR 08-NOV-2002; 2002US-0424894P.  
XX  
PA (NEOS-) NEOSE TECHNOLOGIES INC.  
XX  
PI Johnson KF, Bezila DJ;  
XX  
DR WPI; 2004-132958/13.  
DR N-PSDB; ADJ27350.  
XX  
PT Producing fucosylated glycoprotein, by contacting recombinant  
PT fucosyltransferase protein with mixture comprising donor substrate and  
PT acceptor substrate on glycoprotein.  
XX  
PS Claim 1; Fig 4; 84pp; English.  
XX  
CC This sequence represents an alpha-1,3/4-fucosyltransferase protein which  
CC was used in the method of the invention for producing a fucosylated  
CC glycoprotein. The method involves contacting a recombinant  
CC fucosyltransferase protein with a mixture comprising a donor substrate  
CC which comprises a fucosyl residue, and an acceptor substrate on a  
CC glycoprotein, under conditions such that the fucosyltransferase protein  
CC catalyzes the transfer of the fucose residue from a donor substrate to  
CC the acceptor substrate on the glycoprotein. The method is useful for  
CC producing fucosylated glycoprotein.  
XX  
SQ Sequence 277 AA;

Query Match 15.2%; Score 68; DB 8; Length 277;  
Best Local Similarity 100.0%; Pred. No. 1.5e-57;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 73 NPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRYLRMPLYYDRLHHK 132  
Db 74 NPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRYLRMPLYYDRLHHK 133  
  
Qy 133 AESVNDDTT 140  
Db 134 AESVNDDTT 141  
<!--EndFragment-->

<!--StartFragment-->RESULT 7  
ADJ77810  
ID ADJ77810 standard; protein; 486 AA.  
XX  
AC ADJ77810;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Helicobacter pylori strain 1182 FutB protein SeqID 2.  
XX  
KW FutA; FutB; alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid;  
KW fucose; N-acetylglucosamine; glycoconjugate; enzyme.  
XX  
OS Helicobacter pylori.  
XX  
PN WO2004009838-A2.  
XX  
PD 29-JAN-2004.  
XX  
PF 23-JUL-2003; 2003WO-US023057.  
XX  
PR 23-JUL-2002; 2002US-0398156P.  
PR 08-NOV-2002; 2002US-0424894P.  
XX  
PA (NEOS-) NEOSE TECHNOLOGIES INC.  
XX  
PI Johnson KF, Bezila DJ;  
XX  
DR WPI; 2004-123401/12.  
DR N-PSDB; ADJ77809.  
XX  
PT New isolated polynucleotide encoding fucosyltransferase protein, useful  
PT for synthesizing oligosaccharide moiety on a protein or lipid that is  
PT unglycosylated in its native form or for synthesizing glycolipids.  
XX  
PS Claim 16; SEQ ID NO 2; 72pp; English.  
XX  
CC This invention relates to novel isolated polynucleotides and the encoded  
CC polypeptides thereof, which are related to the fucosyltransferase enzymes  
CC (FutA and FutB) of Helicobacter pylori (H. pylori). Specifically, it  
CC refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to  
CC chemically synthesise glycoproteins and glycolipids with the desired  
CC oligosaccharide moieties (i.e. by transfer of a fucose residue to N-  
CC acetylglucosamine), such that they are useful in the preparation of  
CC glycoconjugates. The present invention describes how bacterial  
CC fucosyltransferase is unaffected by the sialylation status of the acceptor  
CC sugar, as opposed to the mammalian homologue, and furthermore,  
CC bacterially expressed enzymes offer a large cost saving relative to  
CC mammalian expression systems. This polypeptide sequence is an H. pylori  
CC strain 1182 FutB protein sequence of the invention.  
XX  
SQ Sequence 486 AA;

Query Match 13.2%; Score 59; DB 8; Length 486;  
Best Local Similarity 100.0%; Pred. No. 1.6e-48;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 366 DDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLELSQNT 424  
Db 400 DDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLELSQNT 458

<!--EndFragment-->

<!--StartFragment-->ADJ27345  
ID ADJ27345 standard; protein; 486 AA.  
XX  
AC ADJ27345;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Alpha-1,3/4-fucosyltransferase.  
XX  
KW alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase;  
KW fucosyl; fucose.  
XX  
OS Helicobacter pylori; strain 1182 FutB.  
XX  
PN WO2004009793-A2.  
XX  
PD 29-JAN-2004.  
XX  
PF 23-JUL-2003; 2003WO-US023155.  
XX  
PR 23-JUL-2002; 2002US-0398156P.  
PR 08-NOV-2002; 2002US-0424894P.  
XX  
PA (NEOS-) NEOSE TECHNOLOGIES INC.  
XX  
PI Johnson KF, Bezila DJ;  
XX  
DR WPI; 2004-132958/13.  
DR N-PSDB; ADJ27344.  
XX  
PT Producing fucosylated glycoprotein, by contacting recombinant  
PT fucosyltransferase protein with mixture comprising donor substrate and  
PT acceptor substrate on glycoprotein.  
XX  
PS Claim 1; Fig 1; 84pp; English.  
XX  
CC This sequence represents an alpha-1,3/4-fucosyltransferase protein which  
CC was used in the method of the invention for producing a fucosylated  
CC glycoprotein. The method involves contacting a recombinant  
CC fucosyltransferase protein with a mixture comprising a donor substrate  
CC which comprises a fucosyl residue, and an acceptor substrate on a  
CC glycoprotein, under conditions such that the fucosyltransferase protein  
CC catalyzes the transfer of the fucose residue from a donor substrate to  
CC the acceptor substrate on the glycoprotein. The method is useful for  
CC producing fucosylated glycoprotein.  
XX  
SQ Sequence 486 AA;  
  
Query Match 13.2%; Score 59; DB 8; Length 486;  
Best Local Similarity 100.0%; Pred. No. 1.6e-48;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 366 DDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLELSQNT 424  
Db 400 DDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLELSQNT 458  
<!--EndFragment-->